

WHAT IS CLAIMED IS:

1. An isolated polynucleotide from coryneform bacteria, containing a polynucleotide sequence, selected from the group consisting of
- 5 a) polynucleotide which is at least 70 % identical to a polynucleotide coding for a polypeptide which contains the amino acid sequence of SEQ ID no. 2,
- 10 b) polynucleotide which codes for a polypeptide containing an amino acid sequence which is at least 70 % identical to the amino acid sequence of SEQ ID no.2,
- c) polynucleotide which is complementary to the polynucleotides of a) or b), and
- 15 d) polynucleotide containing at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c).
2. A polynucleotide as claimed in claim 1, wherein the polynucleotide is a DNA, preferably recombinant, which
- 20 can be replicated in coryneform bacteria.
3. A polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.
4. A replicable DNA as claimed in claim 2, containing
- i) the nucleotide sequence shown in SEQ ID no. 1, or
- 25 ii) at least one sequence which corresponds to the sequence (i) within the degeneracy region of the genetic code, or

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iii) at least one sequence which hybridises with the sequence complementary to sequence (i) or (ii), and optionally

iv) functionally neutral sense mutations in (i).

5 ^{5.}~~6.~~ A polynucleotide sequence as claimed in claim 2, which codes for a polypeptide containing the amino acid sequence shown in SEQ ID no. 2.

^{6.}~~7.~~ A vector containing a polynucleotide sequence as claimed in claim 1.

10 ^{7.}~~8.~~ A coryneform bacterium containing a vector as claimed in claim 6.

^{8.}~~9.~~ A process for the fermentative preparation of L-amino acids, wherein the following steps are carried out:

15 a) Fermentation of coryneform bacteria producing the L-amino acid in which at least the gene coding for component H of the phosphotransferase system is enhanced, particularly overexpressed,

b) Enrichment of the L-amino acid in the medium or in the cells of the bacteria and

20 c) Isolation of the L-amino acid.

^{9.}~~10.~~ A process as claimed in claim 9, wherein bacteria are used in which, in addition, further genes of the biosynthesis pathway of the desired L-amino acid are enhanced.

25 ^{10.}~~11.~~ A process as claimed in claim 9, wherein bacteria are used in which the metabolic pathways which reduce the formation of the L-amino acid are at least partially excluded.

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11.
12. A process as claimed in claim 9, wherein a strain transformed with a plasmid vector is used and the plasmid vector carries the nucleotide sequence of the gene coding for component H of the phosphotransferase system.
- 5
12.
13. A process as claimed in one or more of claims 9 to 12, wherein coryneform bacteria which produce L-lysine are used.
13.
14. A process as claimed in claim 10, wherein one or more of the genes selected from the group consisting of
- 10 the dapA gene coding for dihydrodipicolinate synthase, the pyc coding for pyruvate carboxylase, the tpi gene coding for triosephosphate isomerase, the gap gene coding for glyceraldehyde-3-phosphate dehydrogenase,
- 15 the ptsM gene coding for component M of the phosphoenolpyruvate-sugar-phosphotransferase system (ptsM) the pgk gene coding for 3-phosphoglycerate kinase, and
- 20 the lysE gene coding for lysine export, are simultaneously enhanced, particularly overexpressed or amplified.
14.
15. A process as claimed in claim 11, wherein, for the production of L-lysine, bacteria are fermented in which one or more of the genes selected from the group consisting of
- 25 the pck gene coding for phosphoenolpyruvate carboxylase,

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the *pgi* gene coding for glucose-6-phosphate isomerase,
the *poxB* gene coding for pyruvate oxidase
are simultaneously attenuated.

15.
16. The process as claimed in one of claims 9-12 or 14-15,
5 wherein microorganisms of the *Corynebacterium*
glutamicum genus are used.

16.
17. The use of polynucleotide sequences as claimed in
claim 1 as primers for the preparation of the DNA of
genes which code for the *ptsH* gene product, by the
10 polymerase chain reaction.

17.
18. The use of polynucleotide sequences as claimed in
claim 1 as hybridisation probes.

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